WHAT IS CLAIMED IS:

1. A bacteriophage library useful for typing bacteria, the bacteriophage library comprising a plurality of bacteriophages being categorized into:

(a) a first category including bacteriophages being infective to a first type of bacteria;

(b) a second category including bacteriophages being infective to a second type of bacteria; and

(c) a third category including bacteriophages being infective to both said first type and said second type of bacteria.

2. The bacteriophage library of claim 1, wherein the library is provided as an array, such that each of said plurality of bacteriophages occupies a specific location of said array.

3. The bacteriophage library of claim 2, wherein said plurality bacteriophages of said array are each provided in a liquid medium.

4. The bacteriophage library of claim 3, wherein said liquid medium is capable of supporting bacterial growth.

5. The bacteriophage library of claim 2, wherein said plurality of bacteriophages of said array are each attached to a solid support.

6. The bacteriophage library of claim 5, wherein said solid support is selected from the group consisting of a membrane, an agar plate and a microtiter plate.

7. The bacteriophage library of claim 1, wherein said library includes mutants of known bacteriophages said mutants being characterized by bacterial host specificity different than said known bacteriophages.

8. The bacteriophage library of claim 1, wherein said first type and said second type of bacteria are each bacteria responsible for a food borne disease.

9. The bacteriophage library of claim 1, wherein said first type and said second type of bacteria are each of a bacterial genus selected from the group consisting of *Salmonella*, *Staphylococcus*, *Streptococcus*, *Shigella*, *Listeria*, *Campylicbacter*, *Klebsiella*, *Yersinia*, *Pseudomonas* and *Escherichia*.

10. The bacteriophage library of claim 1, wherein said first and said second bacteria types are different bacterial species of the same genus.

11. The bacteriophage library of claim 1, wherein said first and said second bacteria types are different bacterial strains of the same species.

12. The bacteriophage library of claim 1, wherein said first and said second bacteria types are different bacterial serovars of the same strain.

13. The bacteriophage library of claim 1, wherein each of said first, second and third categories include N bacteriophages, whereas N is

an integer selected from the group consisting of integers between and including 2 and 10,000.

14. The bacteriophage library of claim 1, wherein said library is sufficiently diversified bacteriophage content so as to enable the typing of all known constituents of a bacterial genus.

15. A method of typing bacteria present in a sample, the method comprising the steps of:

(a) incubating the sample with an arrayed library of bacteriophages being categorized into:

(i) a first category including bacteriophages being infective to a first type of bacteria;

(ii) a second category including bacteriophages being infective to a second type of bacteria; and

(iii) a third category including bacteriophages being infective to both said first type and said second type of bacteria; and

(b) identifying bacteriophages being infective to at least one bacteria in said sample; and

(c) correlating between an identity of said bacteriophages being infective to said at least one bacteria and an identity of bacteriophages of said library known to be infective to bacterial standards, so as to enable typing of said at least one bacteria present in the sample.

16. The method of claim 15, wherein said step of incubating the sample with said library of bacteriophages is performed in a presence, or with subsequent addition of, an assay reagent for identifying presence

or absence of infection between any specific bacteriophage of said library and bacteria in said sample.

17. The method of claim 16, wherein said assay reagent is a polynucleotide intercalating agent selected from the group consisting of ethidium bromide and propidium iodide.

18. The method of claim 15, wherein said step of incubating the sample with said library of bacteriophages is carried out on or in a medium supporting bacterial growth.

19. The method of claim 18, wherein said medium is selected from the group consisting of a solid medium and a liquid medium.

20. The method of claim 15, wherein said bacteriophage library is provided as a preparation selected from the group consisting of a plurality of individual bacteriophage suspensions, a plurality of freeze dried individual bacteriophage powders and a solid support carrying a plurality of individual bacteriophages.

21. The method of claim 15, wherein said library includes mutants of known bacteriophages, said mutants being characterized by bacterial host specificity different than said known bacteriophages.

22. The method of claim 15, wherein said first type and said second type of bacteria are each bacteria responsible for a food borne disease.

23. The method of claim 15, wherein said first type and said second type of bacteria are each of a bacterial genus selected from the group consisting of *Salmonella*, *Staphylococcus*, *Streptococcus*, *Shigella*, *Listeria*, *Campylicbacter*, *Klebsiella*, *Yersinia*, *Pseudomonas* and *Escherichia*.

24. The method of claim 15, wherein said first and said second bacteria types are different bacterial species of the same genus.

25. The method of claim 15, wherein said first and said second bacteria types are different bacterial strains of the same species.

26. The method of claim 15, wherein said first and said second bacteria types are different bacterial serovars of the same strain.

27. The method of claim 15, wherein each of said first second and third categories include N bacteriophages, whereas N is an integer selected from the group consisting of integers between and including 2 and 10,000.

28. The method of claim 15, wherein said library is of sufficiently diversified bacteriophage content so as to enable the typing of all known constituents of a bacterial genus.

29. A system for typing bacteria present in a sample, the system comprising:

(a) a library of bacteriophages being categorized into:

(i) a first category including bacteriophages being infective to a first type of bacteria;

(ii) a second category including bacteriophages being infective to a second type of bacteria; and

(iii) a third category including bacteriophages being infective to both said first type and said second type of bacteria; and

(b) a detector being for detecting a presence or absence of infection between at least one bacteria in said sample and individual bacteriophages of said library.

30. The system of claim 29, further comprising a processing unit being for comparing said presence or absence of infection as detected by said detector to a presence or absence of infection between bacteriophages of said library and known bacterial standards, so as to enable typing of said at least one bacteria.

31. The system of claim 29, wherein said library is provided as an array such that each of said plurality of bacteriophages occupies a specific location of said array.

32. The system of claim 31, wherein said bacteriophages of said array are each provided in a liquid medium.

33. The system of claim 32, wherein said liquid medium is capable of supporting bacterial growth.

34. The system of claim 31, wherein said bacteriophages of said array are each attached to a solid support.

35. The system of claim 34, wherein said solid support is selected from the group consisting of a membrane, an agar surface, a microtiter plate, beads and optic fibers.

36. The system of claim 29, wherein said library includes mutants of known bacteriophages, said mutants being characterized by bacterial host specificity different than said known bacteriophages.

37. The system of claim 29, wherein said first type and said second type of bacteria are each bacteria responsible for a food borne disease.

38. The system of claim 29, wherein said first type and said second type of bacteria are each of a bacterial genus selected from the group consisting of *Salmonella, Staphylococcus, Streptococcus, Shigella, Listeria, Campylicbacter, Klebsiella, Yersinia, Pseudomonas* and *Escherichia.*

39. The system of claim 29, wherein said first and said second bacteria types are different bacterial species of the same genus.

40. The system of claim 29, wherein said first and said second bacteria types are different bacterial strains of the same species.

41. The system of claim 29, wherein said first and said second bacteria types are different bacterial serovars of the same strain.

42. The system of claim 29, wherein each of said first, second and third categories include N bacteriophages, whereas N is an integer

selected from the group consisting integers between and including 2 and 10,000.

43. The system of claim 29, wherein said library is of sufficiently diversified bacteriophage content so as to enable the typing of all known constituents of a bacterial genus.

44. The system of claim 29, wherein said detector is capable of visually detecting plaques.

45. The system of claim 29, wherein said detector is capable of detecting a presence of released bacterial constituent associated with bacterial lysis.

46. A method of uncovering mutant bacteriophages useful in typing bacteria, the method comprising the steps of:

(a) providing a sample of bacteriophages at a first routine titer dilution;

(b) concentrating said sample of bacteriophages to a second routine titer dilution, said second routine titer dilution being more concentrated than said first routine titer dilution;

(c) infecting a first bacterial sample with said sample of bacteriophages from step (a);

(d) infecting a second bacterial sample identical to said first bacterial sample with said sample of bacteriophages resultant from step (b); and

(e) only if said second bacterial sample is lysed, whereas said first bacterial sample is not, isolating bacteriophages from said second bacterial sample, thereby uncovering mutant

bacteriophages useful in typing bacteria of said bacterial samples.

47. An array of bacteriophages useful for typing bacteria, the array comprising a plurality of distinct bacteriophages each occupying a distinct location of said array, at least a portion of said plurality of distinct bacteriophages being capable of infecting more than one bacterial host type.

48. The array of claim 47, wherein said plurality of distinct bacteriophages are attached to a solid support.

49. The array of claim 47, wherein said plurality of bacteriophages are categorized into:

(a) a first category including bacteriophages being infective to a first type of bacteria;

(b) a second category including bacteriophages being infective to a second type of bacteria; and

(c) a third category including bacteriophages being infective to both said first type and said second type of bacteria

50. A method of typing bacteria, the method comprising the steps of:

(a) providing an array of bacteriophages including a plurality of distinct bacteriophages each occupying a distinct location of said array, at least a portion of said plurality of distinct bacteriophages capable of infecting more than one bacterial host type;

(b) reacting said array of bacteriophages with a bacterial sample so as to produce a first pattern of bacterial plaques on said array; and

(c) comparing said first pattern to patterns of bacterial plaques resultant from reacting said array of bacteriophages with known bacterial samples, so as to enable typing of said bacterial sample.